

GenCore version 5.1.6
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SUMMARIES

and is derived by analysis of the total score distribution.

OW protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 17:21:34 ; Search time 256 Seconds

(without alignments)
3690.638 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDKALSLSLNDFASISFAE.....LENKINIILSETDRDPIQVY 350

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US09745506/runat.22082003_104400.7027/apf-query.fasta.1.519
-DB=N.Geneseq.19Jun03 -QFWT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEDUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq.19Jun03:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

Result No.	Score	Query Match	Length	DB	ID	Description
1	1799	100.0	1053	22	AAH52212	Human AFP protein
2	1799	100.0	1574	22	AAH16397	Human CDNA sequenc
3	1799	100.0	1636	22	AAK60866	Human Immune/haema
4	1799	100.0	1739	23	ABV23243	Human prostate exp
5	1799	100.0	1739	23	ABV29087	Human prostate exp
6	1793	99.7	1554	22	AA544644	Human full-length
7	1763	98.0	1398	22	AA599945	Human gene express
8	1725.5	95.9	1385	24	AB60919	Human protein kina
9	1209.5	67.2	1686	23	AA585172	DNA encoding novel
10	826.5	45.9	796	22	AAH07192	Human CDNA clone (
11	737	41.0	14969	22	AAK78763	Human Immune/haema
12	644	35.8	462	22	AAI23953	Human breast cance
13	602	33.5	514	22	AAI15105	Human breast cance
14	578	32.1	1011	23	ABJ07427	Drosophila melanog
15	578	32.1	2967	23	ABL10022	Drosophila melanog
16	578	32.1	3011	22	AA544816	Human contig polyn
17	538	29.9	513	22	AA544816	Bovine EST associa
18	467	26.0	394	25	ABX45683	Human breast cell
19	391	21.7	465	22	ABA57019	Human foetal liver
20	391	21.7	465	22	AAK05073	Human brain expres
21	391	21.7	465	22	AAI15235	Probe #5168 for ge
22	391	21.7	465	22	AAI04973	Probe #4964 used t
23	391	21.7	465	22	ABS30297	Human liver single
24	391	21.7	465	22	AAI25260	Human secreted pro
25	366	21.5	249	21	AAI25260	Human breast cell
26	370	20.6	208	22	ABA51524	Human foetal liver
27	370	20.6	208	22	ABA69581	Human brain expres
28	370	20.6	208	22	AAK17792	Human brain expres
29	370	20.6	208	22	AAI24414	Probe #14347 for g
30	370	20.6	208	22	AAI09950	Probe #9941 used t
31	370	20.6	208	22	ABS43283	Human liver single
32	362	20.1	495	23	AA585169	DNA encoding novel
33	330	18.3	633	22	AA534287	Human CDNA encodin
34	305	17.0	1104	24	ABN91378	Staphylococcus epi
35	305	17.0	1104	22	AAH55004	S. epidermidis gen
36	300	16.7	4159	20	AAI12944	Enterococcus faeca
37	300	16.7	4159	24	AB598739	S. epidermidis ope
38	296	16.5	522	23	AA533778	DNA encoding novel
39	291	16.2	522	23	AA585171	Propionibacterium
40	289.5	16.1	3408	23	AA595366	S. epidermidis gen
41	288	16.0	3441	22	AAH54443	Listeria innocua c
42	256	14.2	495269	24	ABO67195	Listeria innocua c
43	256	14.2	3011308	24	ABO69245	S. epidermidis ope
44	249	13.8	1131	22	AAH53356	S. epidermidis gen
45	249	13.8	3014	22	AAH54966	S. epidermidis gen

ALIGNMENTS

RESULT 1
ID AAH52212 standard; CDNA; 1053 BP.

AAH52212:
10-SEP-2001 (first entry)

Human AFP protein encoding CDNA sequence SEQ ID NO:239.

Human: secreted protein; secretion; bacterial cell; fungal cell;
eukaryotic cell; fusion protein; maltose binding protein;
immunoglobulin constant region; polystyridine tag; ss.

OS Homo sapiens.
XX
XX WO200129221-A2.
PN

XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

PS c1a1n 8; SEQ ID 15359; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13633 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 1574 BP; 420 A; 361 C; 372 G; 421 T; 0 other;

Alignment Scores:

Pred. No.: 4,62e-178 Length: 1574
Score: 1799.00 Matches: 350
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-745-506-37 (1-350) x AAH16397 (1-1574)

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DB 271 ATGGATTGTAAGGCTCTCTTCTTCTGTAATGACTTGGCACTCCCTCTGTTGCTGAG 330
QY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
DB 331 AGTTGGACAAATGTTGATTACTGTGGGAACCAAGCCACACATCACTGTAATATACACTC 390
QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAlaAsp 60
DB 391 TTCCTACCAATGACCTGACTGAGGAGTGAAGAGGAGTGTGCAAAAGAGGACGAC 450
QY 61 LeuIleLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTPAsnThr 80
DB 451 CTCATTCTCTCCACATCGGCTATCTTCGACCATGAAGGACATTAACCTGGAACACA 510
QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
DB 511 TGGNAGGACGCGCTGTGATCCGCGCTGGAGAACAGAGTGGTATCTACTCTCCAT 570
QY 101 ThrAlaTyrAspAlaIleProGlnGlyValAsnAspTrpLeuAlaLysGlyLeuGlyAla 120
DB 571 AAGGCTTAATGATGCTGCGCCGAGGCGTCAACACACTGGTGGCTAAAGGCGTTGGAGCT 630
QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
DB 631 TGTACTCCAGGCGCATACATCTTCCAAAGCTCCCACTACCTTACAGAGGAAACACAC 690
QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
|||||

DB 691 CGAGTAGAATTCACGTTAATACACCAAGACCTGGACAAAGTATGTCGACGTGAAA 750
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyLysGlnGluGlnThr 180
DB 751 GGAAATGAGGCTTCTCTGCTCACTCTTTTTCGTGAGACTGTGATGAGAAACAAA 810
QY 181 ArgIleAsnLeuAsnTyrThrGlnLysAlaLeuMetGluValValAspPheLeuSerArg 200
DB 811 CGATTAAATCTGAATTTGTTACTCAGAGGCTTTGATCAGAGTGTACATTTCTTCCCG 870
QY 201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
DB 871 AACAAACACTTATATCAGAAAGACGAAATCTGTCACTGGAGAAAGCCTTGTCTACAT 930
QY 221 ThrGlyMetGlyArgLeuGlySerThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
DB 931 ACTGGAATGGAGGCTTATATGACACATGATGATGTCTCCCTGGCAACCATGATGTGAT 990
QY 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
DB 991 CGAATTAAGAACACCTTAACATATCTCATATTCGCTTACCCCTTGGGGGAGAACAC 1050
QY 261 LeuGluSerGlnValLysValAlaAlaLeuCysAlaGlySerGlySerValLeuGln 280
DB 1051 TTGAGCTCTCAAGTCAAGACGCGCCCTGTGTGTCTGTGGAGACGCTTCTGACG 1110
QY 281 GlyValGluAlaAspLeuTyrThrGlnGlyMetSerHisAspThrLeuAspAla 300
DB 1111 GGTGTGAGGCTGACCTTATCTACACAGGAGTGAATGTCCTCATATATCTTGGATGCT 1170
QY 301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgIlePheLeu 320
DB 1171 GCTTCCCAAGGATTAATGTCATCTCTGTGGAACACAGACACTGACAGGCTTCTCT 1230
QY 321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleLeuSer 340
DB 1231 TCTGACCTTCGAAATATGCTGGATTTCTCACTTGGAGAAATATATATATATCATCA 1290
QY 341 GluThrAspArgAspProLeuGlnValVal 350
DB 1291 GAGACTGACAGGAGCCCTCTTCAGGTGCTA 1320

RESULT 3
AAK60866
ID AAK60866 standard; cDNA; 1696 BP.
XX
AC AAK60866;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen encoding cDNA SEQ ID NO:5926.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
PD 09-AUG-2001.
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184654.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.

PR	30-JUN-2000	2000US-0215135
PR	07-JUL-2000	2000US-0216647
PR	07-JUL-2000	2000US-0216880
PR	11-JUL-2000	2000US-0217487
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PR	20-OCT-2000;	2000US-02411808.
PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
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PR	08-NOV-2000;	2000US-0246475.
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PR	17-NOV-2000;	2000US-0249300.
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PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
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PR	05-JAN-2001;	2001US-0259678.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI: 2001-483426/52.	
XX	P-PSDB; AAM80805.	
XX		
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
XX		
PS	Claim 1; SEQ ID NO 5926; 3071pp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)	
CC	amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	

expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent
 CC diagnosis and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.

XX Sequence 1696 BP; 510 A; 369 C; 379 G; 435 T; 3 other;

Alignment Scores:

Pred. No.: 5,15e-178 Length: 1696
 Score: 1799.00 Matches: 350
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-745-506-37 (1-350) x AAK60866 (1-1696)

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 DB 307 ATGGAATTGAAGCGCTCTCTTCTTCTTGAATGATTTGCAATCCCTTCGTTGGTGAG 366
 OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 DB 367 AGTTGGGACAAATGTTGATTTACTGTGGAGAACCAAGCCCAACATCTGTAATATACATC 426
 OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
 DB 427 TTCGTGACCAATGACTGACTGAGAGAGATGAGAGAGAGTCTGCAAAAGAGGACAGAC 486
 OY 61 LeuIleLeuSerThrHisProProIlePheArgProMetLysArgIleThrTPAsnThr 80
 DB 487 CTCATCTCTCTTACCATCCGCTTATCTCCGACCATGAGGAGCATATACCTGAGACACA 546
 OY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
 DB 547 TGGAGAGAGCGCTGGTATCCGGGCTGGAGAACAGAGTGGTCTACTCTCTCCAT 606
 OY 101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
 DB 607 ACAGCCTATGATGCTGCGCCCGCCAGGCGCTCAACAACTGGTGGCTTAAGGCTTGAGCT 666
 OY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrgLysAsnHis 140
 DB 667 TGTACTCCAGGCGCCATACATCTTCCAAAGCTCCCAACTACCTACAGGGGAAACAC 726
 OY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
 DB 727 CGAGTAGAATTCACGTTACTACACCCCAAGACCTGGACAAAGTCAATGTGTGAGTGA 786
 OY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThr 180
 DB 787 GGAATTTGACGGTGTCTCTCACTTTTCTGCTGAGACCTGGTAATAGGAACAACA 846
 OY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGluValValAspPheLeuSerArg 200
 DB 847 CGGATTAATCTGATCTACTCAGAAAGCTTTGATCCAGCTGTAGATTTCTTTCCCG 906
 OY 201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
 DB 907 AACCAACAACTTATCAGAAAGACGGAATTTCTGCTACTGGAGAACCTTTGCTTCAAT 966
 OY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetLeuAsp 240
 DB 967 ACTGGATGGAGCGGTTATGACACACTGGATGAATCTGCTCCCTGGCAACCAAGATGAT 1026
 OY 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyAlaGlyArgThr 260

DB 1027 CGAATTAAGAACACTAAACTATCTCATATCTGCTTACCCCTGGGGTGGAGAAC 1086
 OY 261 LeuGluSerGlnValLysValAlaAlaLeuCysAlaGlySerGlySerValLeuGln 280
 DB 1087 TTAGAGCTTCACGTCAAGTCAAGTCCGCTGTGTGCTGGTTCGGAGCGCTTCGCA 1146
 OY 281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
 DB 1147 GCGTTGAGCGCTACCTTTTACCTCACAGGTGAGATGTCCTCATCATATCTTGGATGCT 1206
 OY 301 AlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGluArgLysPheLeu 320
 DB 1207 GCTTCCCAAGAAATAATGTCATCTCTGGAACACAGACACACTGAGAGGCTTTCTT 1266
 OY 321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleLeuSer 340
 DB 1267 TCTGACCTTCGAAATGTGCTGATTTCTCACTTGGAGAAATTAATTAATTAATCA 1326
 OY 341 GluThrAspArgAspProLeuGlnValVal 350
 DB 1327 GAGACTGACAGGAGCCCTTTCAGTGTGTA 1356

RESULT 4
 ABV23243
 ID ABV23243 standard; cDNA; 1739 BP.
 XX
 AC ABV23243:
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 23234.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 PN MO200160860-A2.
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 DR
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 4189-4190; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1739 BP; 457 A; 389 C; 411 G; 473 T; 9 other;

Alignment Scores:

Pred. No.:	5,34e-178	Length:	1739
Score:	1799.00	Matches:	350
Percent Similarity:	100.008	Conservative:	0
Best Local Similarity:	100.008	Mismatches:	0
Query Match:	100.008	Indels:	0
DB:	23	Gaps:	0

US-09-745-506-37 (1-350) x ABV23243 (1-1739)

```
QY 1 MetAspLeuLysAlaLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
    |||
DB 297 ATGATTTGAAGGCTCTCTTCTTCTTGAATGACTTGGATCCCTCGTTTGTCTGAG- 356
    |||
QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProHisThrValAsnThrLeu 40
    |||
DB 357 AGTGGGACAAATGTTGATTTACTGTTGACCAAGCCACACACTACTGTAATACACTC 416
    |||
QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluLysAlaAsp 60
    |||
DB 417 TTCTGTGACCAATGACCTGAGCTGAGAGAGATGAGAGAGTGTGCAAAAGAGCAGAC 476
    |||
QY 61 LeuLeuLeuSerTrpHisProProLeuPheArpProMetLysArgGlyLeuThrAsnThr 80
    |||
DB 477 CTCAATCTCTCTACCAATCCGCTATCTCCGACCCATGAAAGCCATTAACCTGAGACCA 536
    |||
QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyLeuSerProHis 100
    |||
DB 537 TGAAGAGAGCGCCGTGGATCCGGGCTGTGAGAAACAGATCGGTACTCTCCCAT 596
    |||
QY 101 ThrIleArgAspAlaIleProGluGlyAlaAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
    |||
DB 597 ACACCCATGATGATGCTGGCCGCCAGGGGCTCAACAACTGTTGAGGCTTGGAGCT 656
    |||
QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTrpProThrGluGlyAsnHis 140
    |||
DB 657 TGTACTCTCCAGGCCCATACATCTCTCCAAAGCTCCCAACTACCTACAGAGGAAACAC 716
    |||
QY 141 ArgValGluPheAsnValAsnTrpThrGluAspLeuAspLysValMetSerAlaValLys 160
    |||
DB 717 CGAGTAGAATTCACAGTTTACACTACACCCAGACCTGGACAAAGTCATGTGCAGTGAA 776
    |||
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluThr 180
    |||
DB 777 GGAATTTGACGGTGTCTTGTGTCACCTTCTTCTGTAGAGCTGGTAAAGAGAACAAACA 836
    |||
QY 181 ArgIleAsnLeuAsnCysThrGluLysAlaLeuMetGluValValAspPheLeuSerArg 200
    |||
DB 837 CGGATTAATCTGAAATTTGACTCAGAGAGCTTTGATGAGGATGATTTCTTCCCGG 896
    |||
QY 201 AsnLysGluLeuTrpGluLysThrGluLysLeuSerLeuGluLysProLeuLeuLeuHis 220
    |||
DB 897 AACAAACAACTTTATCAGAGAGAGGAAATTTCTGTACAGAGAACCTTTGCTTACAT 956
    |||
QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaIleThrMetLysP 240
    |||
DB 957 ACTGGAAATGAGAGCGGTTTGTGACACTGATGATGATGTCCTCCGTGGCAACCATGTTAT 1016
    |||
QY 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgIleAlaLeuGlyValGlyArgThr 260
    |||
DB 1017 CGAATTAAGAGACACTTAAACTATCTCATATTCCTTACGCCCTTGGGGTGGGAGAAC 1076
    |||
QY 261 LeuGluSerGluValLysValValAlaLeuCysAlaGlySerGlySerValLeuGlu 280
    |||
DB 1077 TTAGAGTCTCAAGTCAAGGTGTGCTGCTGTGTGTTGGGAGCAGGCTTGTGCAG 1136
    |||
```

```
QY 281 GlyValGluAlaAspLeuTrpLeuThrGlyGluMetSerHisHisAspThrLeuAspAla 300
    |||
DB 1137 GGTGTTGAGGCTACCTTACTCTACAGGAGATGTCATCATGATGATCTTGGATGCT 1196
    |||
QY 301 AlaSerGlnGlyLysAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPheLeu 320
    |||
DB 1197 GCTTCCCAAGCAATTAATGTCATCTCTGTGAACACAGCAACTGACAGAGGCTTTCTT 1256
    |||
QY 321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleLeuSer 340
    |||
DB 1257 TCTGACCTTGGAGATATGCTGATTCCTCACTTGGAGAAATGAATATATATCTATCA 1316
    |||
QY 341 GluThrAspArgAspProLeuGluValVal 350
    |||
DB 1317 GAGACTGACAGAGGACCTCTTCAGTGTGTA 1346
    |||
```

RESULT 5

ABV29087
ID ABV29087 standard; cDNA: 1739 BP.

AC ABV29087;

DE 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 29078.

DE Human, prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.

OS Homo sapiens.

PN W0200160860-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-US05171.

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

PS WPI: 2001-662795/76.

DR The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 1739 BP; 457 A; 389 C; 411 G; 473 T; 9 other;

Alignment Scores:

Pred. No.: 5,34e-178
 Score: 1799.00
 Percent Similarity: 100.008
 Best Local Similarity: 100.008
 Query Match: 100.00%
 DB: 23
 Gaps: 0

US-09-745-506-37 (1-350) x ABV29087 (1-1739)

QY 1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
 Db 297 ATGATTTGAAGGCTCTCTTCTTCTTGAATGACTTTGCACTCTCTCTTCTGCTGAG 356
 QY 21 SerTrpAspAsnValLysLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
 Db 357 AGTTGGGACAAATGTTGATTAAGTGGTGAACCAAGCCACACATGATCTGAATACACTC 416
 QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAlaAsp 60
 Db 417 TTCCTACCAATGACTGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 QY 61 LeuLeuLeuSerTrpHisProProLeuPheArgProMetLysArgLleThrTrpAsnThr 80
 Db 477 CTCATCTCTCTCCACATCGGCTATCTTCCGACCATGAGAGGCAATACCTGGAACACA 536
 QY 81 TrpLysGluArgLeuValLleArgAlaLeuGluAsnArgValLleTyrSerProHis 100
 Db 537 TGGAG 596
 QY 101 ThrAlaTyrAspAlaAlaProGlnGluValAsnAsnTrpLeuAlaLysGluAla 120
 Db 597 ACAGGCTATGATCTCTGCGCCCGAGGCGTCAACACATGGTGGCTTAAGGCTTGGAGCT 656
 QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTrpProThrGluGluAsnHis 140
 Db 657 TGTACTCCAGGCGCCATCATCTCTCCAAAGCTCCCAACATACCTACAGAGGAGAACAC 716
 QY 141 ArgValGluPheAsnValAsnTrpThrGlnAspLeuAspLysValMetSerAlaValLys 160
 Db 717 CGAGTGAATTCACCTTACCTACACCAAGACCTGGACAAATCATGTCGACAGTGA 776
 QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrLysGlnGluGlnThr 180
 Db 777 GGAATGACGGGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 836
 QY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArg 200
 Db 837 CGGATTAATCTGAATGTACTCTGAGAGGCTTGTGATGAGTGTGATTTCTTCCCGG 896
 QY 201 AsnLysGlnLeuTrpGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuHis 220
 Db 897 AACCAACCACTTATATGAGAGAGGAAATCTGTCTACTGAGAGAGGCTTGTCTTACAT 956
 QY 221 ThrGlyMetGlyArgLeuCysThrIleAspArgLysValSerLeuAlaTrpMetLleAsp 240
 Db 957 ACTGGAAATGAGAGGCTTATGACACACTGATGAATCTGTCTCTCTGGAACCAATGAT 1016
 QY 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGluValGlyArgThr 260
 Db 1017 CGAATTAATAAGACACCTAAATATCTCATATTCGCTTGGGCTTGGGGAGGAGAAC 1076
 QY 261 LeuGluSerGlnValLysValAlaAlaLeuCysAlaGlySerGlySerValLeuGln 280
 Db 1077 TTAGACTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1136
 QY 281 GlyValGluAlaAspLeuTrpLeuThrGluMetSerHisIleAspThrLeuAspAla 300
 Db 1137 GGGTGTGAGGCTACCTTATCTCAACAGGAGATGATCCCATATATATATTTGGAGTCT 1196
 QY 301 AlaSerGlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgLysPheLeu 320

Db 1197 GCTTCCCAAGGATTAATGCTATCTCTGGAACACAGCAACACTGAAAGGCTTCTT 1256
 QY 321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnLleIleLeuSer 340
 Db 1257 TCTGACCTTGAATATATGCTGATTCACCTTGAAGAAATGAATATATATCTATCA 1316
 QY 341 GluThrAspArgAspProLeuGlnValVal 350
 Db 1317 GAGACTGACAGGAGACCTTCTCAGTGTGTA 1346
 RESULT 6
 AAS44644
 ID AAS44644 standard; DNA; 1554 BP.
 AC AAS44644;
 XX 18-DEC-2001 (first entry)
 DE Human full-length polynucleotide sequence #69.
 XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
 KW cytostatic; antirheumatic; antiarthritic; vulnery; antiinflammatory;
 KW antibacterial; immunosuppressive; vasotropic; antiParkinsonian;
 KW neuroprotective; osteoprotective; antidiabetic; antiallergic; antiallergic;
 KW immunostimulant; analgesic; gene therapy.
 XX Homo sapiens.
 OS
 XX
 PN WC200164834-A2.
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001MO-US04926.
 XX
 XX 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PR 17-JUN-2000; 2000US-0597707.
 PR 14-JUL-2000; 2000US-0616807.
 PR 19-SEP-2000; 2000US-0664641.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao Qa, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 PI Dmanac R;
 XX
 XX WPI: 2001-589862/66.
 DR P-PSDB; AAD27744.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of
 PT cancer, neurological, inflammatory disorders and for use in arrays for
 PT detection -
 XX
 XX Claim 1: SEQ ID NO 69; 153pp; English.
 CC Sequences AAS44576-AAS44919 represent full-length polynucleotides and
 CC contig polynucleotides encoding polypeptides of the invention. The DNA
 CC and protein sequences are useful for the treatment, diagnosis and
 CC prevention of various types of disorder in a mammalian subject such as a
 CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
 CC such as leukemia, lymphoma and neuroblastoma, autoimmune disorders such
 CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
 CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's

Best Local Similarity: 98.87% Mismatches: 0
 Query Match: 98.00% Indels: 3
 DB: 22 Gaps: 0
 US-09-745-506-37 (1-350) x AAF59945 (1-1398)

```

OY 1 MetaspLeuAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB 236 ATGATTTGAAGGCTCTCTCTCTCTGATGATGATTCGATCCCTCGCTTGCTGAG 295
OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
DB 296 AGTTGGGCAATGTGGATTACTGGTGAACCAAGCCACACATCTAATAATACATC 355
OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluInLysAlaAsp 60
DB 356 TTCCGACCAATGACCTGACTGAGAGAGATGAGAGAGTCTGCAAAAGAGGAGAC 415
OY 61 LeuLeuLeuSerThrHisProProIlePheArgProMetLysArgIle-ThrTPAsnTh 80
DB 416 CTCATTCTCTCTTACCATCCGCTATCTCCGACCATGACCATGACCATTAACCTGGAGAC 475
OY 80 rTTP--LysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyTlSerSerPro 99
DB 476 ATGGAGAGGAGCGCGCTGGATCCGCGCTGAGAAACAGATCGGATCTACTCTCTCT 535
OY 100 HisThrAlaTyraAspAlaAlaProGluGluValAsnAsnThrLeuAlaLysGluLeuGly 119
DB 536 CATACAGCCTATGATGCTGCGCCGCCGACGCTACACACTGGTGGCTAAAGGCTTGA 595
OY 120 AlaCysThrSerArgProIleHisProSerLysAlaProAsnTyreProThrGluLysAsn 139
DB 596 GCTTGACTCTCAGGCGCCATACATCTTCCAAAGCTCCCACTACCTGACAGAGGAAC 655
OY 140 HisArgValGluPheAsnValAsnTyThrGlnAspLeuAspLysValMetSerAlaVal 159
DB 656 CACCGAGTGAATTCACCTTAACCTACACCAAGCTGACAAAGTCAATGCTCCAGTGT 715
OY 160 LysGlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlyGluGluGlu 179
DB 716 AAGGATTTGACGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 775
OY 180 ThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSer 199
DB 776 ACACGATTAATCTGAAATGTAAGTCAAGAGGCTTTGATGACAGTGTGATTTCTTTCT 835
OY 200 ArgAsnLysGluLeuTyrglnLysThrGluIleLeuSerLeuGluLysProLeuLeu 219
DB 836 CGGAACAAACAACTTATTCAGAAAGCGGAATTCCTGCTACTGGAGAAAGCTTTGCTTCA 895
OY 220 HisThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIle 239
DB 896 CATCTAGGAATGGAGCGTTATGACACACTGATGAATCTGCTCTCCCTGGCAACCAATG 955
OY 240 AspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValArg 259
DB 956 GATCGAATTAAGAAAGACCTAAACATATCTCAATTCGTTGACCTTGGGGGGGAGAA 1015
OY 260 ThrLeuGluSerGlnValLysValAlaAlaLeuCysAlaGlySerGlySerValLeu 279
DB 1016 ACCTTAGACTCTCAAGTCAAACTCGGCGCTGTGTGCTGTGGGAGACAGCGTTCTG 1075
OY 280 GlnGlyValGluAlaAspLeuThrLeuThrGlyGluMetSerHisHisSphrThrLeuAsp 299
DB 1076 CAGGGGTGTGAGGCTGACCTTTAATCTCAAGGTGACATGATCCCATCATATATCTTGGAT 1135
OY 300 AlaAlaSerGlnGlyLysAsnValIleLeuCysGluHisSerAsnThrGluArgGlyPhe 319
DB 1136 GCTGCTTCCCAAGGAATATGTCATCTCTGTGAACACAGCAACACTGACAGAGGCTTT 1195
OY 320 LeuSerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleLeu 339
DB 1196 CTTTCTGACCTTCGAGATATGCTGATTTCTACTTGGAGAAATGAATATATATATCCCA 1255

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OY 340 SerGluThrAspArgAspProLeuGluValVal 350
 DB 1256 TCGAGACTGACAGGAGCCCTTCTCAGGTGTA 1288

RESULT 8

ABL60919
 ID ABL60919 standard; cDNA; 1385 BP.

AC ABL60919;

DE 23-SEP-2002 (first entry)

DE Human protein kinase C 27.17 polypeptide encoding cDNA.

KW Human; protein kinase C 27.17; protein metabolism; gene; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 389..1132 /tag= a /product= "protein kinase C 27.17 polypeptide"

XX CN1333355-A.

PD 30-JAN-2002.

XX 07-JUL-2000; 2000CN-0117049.

XX 07-JUL-2000; 2000CN-0117049.

PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

XX Mao Y, Xie Y;

XX WPI; 2002-305609/35.

DR P-PSDB; ABB08182.

PT Human protein kinase C 27.17 polypeptide and its encoding

XX polynucleotide, for treating e.g. protein metabolism disturbance -

XX Claim 6; Page 25-26 (disclosure); 33pp; Chinese.

CC The invention relates to a human protein kinase C 27.17 polypeptide and

CC its encoding polynucleotide. The polypeptide can be expressed by standard

CC DNA recombination. The polynucleotide, polypeptide and its antagonist are

CC useful for treating e.g. protein metabolism disturbance. The present

CC sequence represents the human protein kinase C 27.17 polypeptide encoding

CC cDNA.

XX Sequence 1385 BP; 375 A; 324 C; 308 G; 378 T; 0 other;

US-09-745-506-37 (1-350) x ABL60919 (1-1385)

Alignment Scores:

Pred. No.: 1.87e-170 Length: 1385
 Score: 1725.50 Matches: 344
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.29% Mismatches: 5
 Query Match: 95.91% Indels: 2
 DB: 24 Gaps: 0

```

OY 1 MetaspLeuAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB 82 ATGATTTGAAGGCTCTCTCTCTCTGATGATGATTCGATCCCTCGCTTGCTGAG 141
OY 21 SerTPAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeu 40
DB 142 AGTTGGGCAATGTGGATTACTGGTGAACCAAGCCACACATCTAATAATACATC 201
OY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGluInLysAlaAsp 60

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Db      202 TTCTGACCAATGACCTGACTGAGGAAGTGAGAGAGTGCTGCAAAAAGAGGACGAC 261
Qy      61 LeuileuSerTyrHisProPheArgPheArgProMetLysArgIleThrTrpAsnThr 80
Db      262 CTCATTCCTCTCCATCCATCCGCTATCTCGAGCCCATGAGCCCATTAACCTGGACACA 321
Qy      81 TrpYsgluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
Db      322 TGGAGGAGCGCCCGCGGATCCGGGCTCGGAGAACAGAGCGGATCTACTCTCCATCAT 381
Qy      101 ThrIleTyrAspAlaIleProGlnGlyValAsnAsnTrpLeuAlaIleValGlyLeuGlyAla 120
Db      382 ACAGCCTATGATGCTGGCGCCCGAGGGGCTCAACAACGTGGTGGCTAAAGGGCTGGAGCT 441
Qy      121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHis 140
Db      442 TGTACCTCCAGCCATA-CATCTTTCAGAGCT-CCCAACTCCCTCCACAGAGAACCCAC 499
Qy      141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
Db      500 CGAGTAGAATTCACAGCTTAACACCCAGACCTGGGACAAAGTCATGTGCAAGTAA 559
Qy      161 GlyIleAspGlyValSerValThrSerPheSerAlaArgTrpGlyAsnGluGluGlnThr 180
Db      560 GGAATGACGGGTGTTCTGTCACTTCTTCTGCTAGAGCTGTAATGAGAACCAACA 619
Qy      181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSerArg 200
Db      620 CGAATTAATCTGAATTTGTACTCAGAGAGCTTGAATGCGAGGTATGATTTCTTCCCGG 679
Qy      201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGluLysProLeuLeuLeuHis 220
Db      680 AACCAACAACCTTATACAGAACAGCGAAATCTGTCACTGAGAGAGCCCTTCTCTACAT 739
Qy      221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
Db      740 ACTGGAATGGAGCGGTTTGTGACACTGTGATGATCTGCTCCCTGGCAACCATGATTTAT 799
Qy      241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr 260
Db      800 CGAATTAACCAACCTTAACCTATTCATATTCCTTAAGCCCTTGGGGTGGGAGAAC 859
Qy      261 LeuGluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerSerValLeuGln 280
Db      860 TTAGAGTCTCAAGTCAAAGCGTGGCCCTGTGCTGTGGGAGACAGCGTTCTGCAG 919
Qy      281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisIleAspThrLeuAspAla 300
Db      920 GGTTGTGGGCTGACCTTACCTCACAGGTGAGATGTCCCATCATGATTAATCTTGGATCT 979
Qy      301 AlaSerGlnGlyIleAsnValIleLeuGlySerGluHisSerAsnThrGluArgGlyPheLeu 320
Db      980 GCTTCCCAAGAAATTAATGTATCTCTCTGTGACACACACACACAGAGGAGGCTTCTT 1039
Qy      321 SerAspLeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleLeuSer 340
Db      1040 TCTGACCTTCAGATATCTGATTCCTCACTTGGAGATTAAGATTAATATATCTATCA 1099
Qy      341 GluThrAspArgAspProLeuGlnValVal 350
Db      1100 GAGACTGACAGGAGCCCTCTTCAGGTGCTA 1129

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RESULT 9
AAS85172/c
ID AAS85172 standard; cDNA; 1686 BP.

AC AAS85172;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #20976.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

```

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-Oct-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB: ABG20985.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 20976; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 1686 BP; 445 A; 397 C; 391 G; 452 T; 1 other;
XX

```

Alignment Scores:
Pred. No.: 2,366-116 Length: 1686
Score: 1209.50 Matches: 308
Percent Similarity: 83.55% Conservative: 7
Best Local Similarity: 81.70% Mismatches: 32
Query Match: 67.23% Indels: 30
DB: 23 Gaps: 10

US-09-745-506-37 (1-350) x AAS85172 (1-1686)

```

Qy      1 MetAspLeuLys-AlaLeuLeuSerSerLeu-AsnAspPheAla---SerLeuSerPheA 19
Db      1383 ATGATTTGAAAGAGCTCTCTTCTTCTCTGGAATGACCTTGTGATCCCTCTGCTTTG 1324
Qy      19 IagLusertTrpAspAsn---ValGlyLeuLeuVal-GluPro-SerProProHis-ThrY 37
Db      1323 CTGAGAGTTGGGAGACAATGTTGGGATTACGTGGGAGAACGAGCCACACACATTAATG 1264
Qy      37 AlaSn---ThrLeuPheLeuThrAsnAspLeuThrGlu---GluValMetGluGluValL 55
Db      1263 TTAATATACACTCTTCTTCGTGGACCAATGACTGACTGAGGAGAGATGAGGAGAGGTGC 1204

```

OY	55	euglnlylvsy-AlaAspIleuIleuSerIyr-Hispropro-Ilephe-ArgProket	73
Db	1203	TGCAGAAAGAGGAGACACTTATCTCTCTCAACCATCCGGCTTATCTCCGACCCATG	1144
OY	74	Lys--ArgIlethrTrpAsnThrTrp-LysgluArgIleuValIleArgAlaIleuGluAs	92
Db	1143	GAAGGCCCATTAACCCGGGAGACATATGGGAAGAGAGCGCTGGTGAATCCGGCTCTGGAGAA	108
OY	92	narValAlGlyIleIyrSerProHisThrAlaItyrAspAlaAlaProGlnGlyAlaAsnAs	112
Db	1083	CAGAGTGCGATTCACCTCTCCATACAGCCATGATGCTCGGCCGCCAGGCGCTCAACAA	1024
OY	112	nTrpIleuAlaIlysGlyIleuGlyAlaCysThrSerArgProIleHisProSerLysAlaPr	132
Db	1023	CTGGTTGGCTAAAGGCGCTGGAGGCTGTGACTCCAGGCCCATACATCTTCCAAAGCTCC	964
OY	132	oAsnTyTrProThrIleuGlyAsnHisArgValIleIuPheAsnValAsnTyTrhGlnAspIe	152
Db	963	CAACTACCCTTCACAGGGAACCCACCGATGAAATTCACAGCTTAACCTACACCCAAAGACT	904
OY	152	u-AspIysValMetSer-AlaValIysGlyIle-AspIylalSerValIThrSerPheSe	171
Db	903	GGGCAAAAGTCATGTCTGGCAGTGAAGAAATTTGACGGGTCTTCTGCACTCTCTTTTC	844
OY	171	ralaArgThrGlyAsnGluGlnIthrArgIleAsnIleuAsnGlyThrGlnIysAlaIe	191
Db	843	TGCTAGAGACTGGTAAAGAGAAACACCGGATTAATGTAATGTAATCTCAAGAGGCTTT	784
OY	191	uMetGlnValValAspPheIleuSerArgAsnIysGlnIleuTyGlnIysTrhGlnIle	211
Db	783	GATCAGAGTGATGATTTCTTTCTCCGGAAACAACTTTATATCAAGAGAGGAAATTC	724
OY	211	uSerIleuGlnIuIysProIleuIleuHisThrGlyMetGlyArgIleuGlyCysThrIleuAspI	231
Db	723	GTCACCTGGAGAGACCTTGGTTCTTACATACATGGAATGGAGCGTTATGCACACTGGAGTA	664
OY	231	uSerValSerIleuAlaThrMetIleAspArgIleIysArgHisIleuIysIleuSerHisI	251
Db	663	ATCTGTCCTCCCTGGCAACCATGATGATGATGATGATGATGATGATGATGATGATGAT	604
OY	251	eaArgIleuAlaIleuGlyValGlyArgThrIleuGluSerGlnValIysValIAlaIleuCy	271
Db	603	TCGGTTAGCCCTTGGGGTGGGAGAACCTTGAAGTCTCAAGTCACAAAGCTGCGCCCTGTG	544
OY	271	salAGlySer-GlySerSerValIleuGlnGlyValGluAlaAspIeutyIleuThr----	289
Db	543	TGCTGGGTCTCTGGGAGACGACCTTCTGCGAGGGTGTTGAGGGGTGACCTTTACCTCACAG	484
OY	290	--GlyIuMetSerHisIAspThrIleu-AspAlaIAser-GlnGlyIle-AsnVal-	307
Db	483	TAGGTGAGATGTCCCATCATGATATTTTGGGATGTGCTTCCCAAGGATTAATATGCA	424
OY	308	IleIeuCysGlu--HisSerAsnThrGluArgIlyPhe--LeuSerAsp-LeuArgAs	325
Db	423	ATCTCTGTGAAACACGCAACCAACTGAACGAGGCGCTTCTCTTCCTGACCTCCGAGA	364
OY	325	pMetIleuAsp---SerHisIeuGluAsnIlysIleAsnIlelle--LeuSerGluThrAs	343
Db	363	TATGCTCTGGAATCTCACCTTGAGAAATTAATATTAATCCTATCCAGAGACCTGA	304
OY	343	PARGAspProIeu 347	
Db	303	CAGGAGCCCTCTT 291	
RESULT 10			
AAH07192			
ID			
AAH07192 standard; cDNA: 796 BP.			
XX			
AAH07192;			
XX			
26-JUN-2001 (first entry)			
DE			
Human cDNA clone (5'-primer) SEQ ID NO:4027.			

XX		Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss-
KX		
XX	Homo sapiens.	
OS	Epi074617-A2.	
PN	07-FEB-2001.	
PD		
XX	28-JUL-2000; 2000EP-0116126.	
Pf		
XX	29-JUL-1999; 99JP-0248036.	
PR	27-AUG-1999; 99JP-0300253.	
PR	11-JAN-2000; 2000JP-0118776.	
PR	02-MAY-2000; 2000JP-0183767.	
FR	09-JUN-2000; 2000JP-0241899.	
XX	(HELI-) HELIX RES INST.	
PA		
XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;	
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;	
XX	WPI; 2001-318749/34.	
XX		
PT	Primer sets for synthesizing polynucleotides, particularly the 5602	
PT	full-length cDNAs defined in the specification, and for the detection	
PT	and/or diagnosis of the abnormality of the proteins encoded by the	
XX	full-length cDNAs -	
XX		
XX	Claim 1; SEQ ID 4027; 2537PP + CD ROM; English.	
PS		
CC	The present invention describes primer sets for synthesizing 5602	
CC	full-length cDNAs defined in the specification. Where a primer set	
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary	
CC	to the complementary strand of a polynucleotide which comprises one of	
CC	the 5602 nucleotide sequences defined in the specification, where the	
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination	
CC	of an oligonucleotide comprising a sequence complementary to the	
CC	complementary strand of a polynucleotide which comprises a 5'-end	
CC	sequence and an oligonucleotide comprising a sequence complementary to a	
CC	polynucleotide which comprises a 3'-end sequence, where the	
CC	oligonucleotide comprises at least 15 nucleotides and the combination of	
CC	the 5'-end sequence/3'-end sequence is selected from those defined in	
CC	the specification. The primer sets can be used in antisense therapy and	
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,	
CC	particularly full-length cDNAs. The primers are also useful for the	
CC	detection and/or diagnosis of the abnormality of the proteins encoded by	
CC	the full-length cDNAs. The primers allow obtaining of the full-length	
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and	
CC	AAH13633 to AAH18742 represent human cDNA sequences, AAH92446 to	
CC	AAH93893 represent human amino acid sequences; and AAH13629 to AAH13632	
CC	represent oligonucleotides, all of which are used in the exemplification	
XX	of the present invention.	
XX		
XX	Sequence 796 BP; 192 A; 204 C; 202 G; 195 T; 3 other:	
US		
US-09-745-506-37 (1-350) x AAH07192 (1-796)		
Oy	Alignment Scores:	
	Pred. No.: 9, 09e-77 Length: 796	
	Score: 826, 50 Matches: 170	
	Percent Similarity: 96, 59% Conservative: 0	
	Best Local Similarity: 96, 59% Mismatches: 6	
	Query Match: 45, 94% Indels: 3	
DB:	22 Gaps: 0	
Db		
Oy	1 MetAAspleuysAlaleuleuSerSerleuaAnApheAlaSerleuSerPhaAglu 20	
Db	271 ATGAGATTGAAGCCTCTCTTCCTTGCTTGATGACTTTGCATCCCTCTCGTGGAC 330	
Oy	21 SerTPAspaAnValglyleuLeuValGluproSerProPronIsthrValAsnThrleu 40	
Db	331 AGTTGGACAATGTGTGATTACTGGTGGCAACCAACCACACACATACGTAAATACACTC 390	

PR 08-NOV--2000; 2000US-0246526.
PR 08-NOV--2000; 2000US-0246527.
PR 08-NOV--2000; 2000US-0246528.
PR 08-NOV--2000; 2000US-0246532.
PR 08-NOV--2000; 2000US-0246609.
PR 08-NOV--2000; 2000US-0246610.
PR 08-NOV--2000; 2000US-0246611.
PR 08-NOV--2000; 2000US-0246613.
PR 17-NOV--2000; 2000US-0249207.
PR 17-NOV--2000; 2000US-0249208.
PR 17-NOV--2000; 2000US-0249209.
PR 17-NOV--2000; 2000US-0249210.
PR 17-NOV--2000; 2000US-0249211.
PR 17-NOV--2000; 2000US-0249212.
PR 17-NOV--2000; 2000US-0249213.
PR 17-NOV--2000; 2000US-0249214.
PR 17-NOV--2000; 2000US-0249215.
PR 17-NOV--2000; 2000US-0249216.
PR 17-NOV--2000; 2000US-0249217.
PR 17-NOV--2000; 2000US-0249218.
PR 17-NOV--2000; 2000US-0249244.
PR 17-NOV--2000; 2000US-0249245.
PR 17-NOV--2000; 2000US-0249264.
PR 17-NOV--2000; 2000US-0249265.
PR 17-NOV--2000; 2000US-0249297.
PR 17-NOV--2000; 2000US-0249299.
PR 17-NOV--2000; 2000US-0249300.
PR 01-DEC--2000; 2000US-0250160.
PR 01-DEC--2000; 2000US-0250391.
PR 05-DEC--2000; 2000US-0251030.
PR 05-DEC--2000; 2000US-0251988.
PR 05-DEC--2000; 2000US-0256719.
PR 06-DEC--2000; 2000US-0251479.
PR 08-DEC--2000; 2000US-0251856.
PR 08-DEC--2000; 2000US-0251868.
PR 08-DEC--2000; 2000US-0251869.
PR 08-DEC--2000; 2000US-0251989.
PR 08-DEC--2000; 2000US-0251990.
PR 11-DEC--2000; 2000US-0254097.
PR 05-JAN--2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

XA Rosen CA, Barash SC, Ruben SW;
PI
XX WPT; 2001-483426/52.
DR

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PS
XX Disclosure; SEQ ID NO 33575; 3071pp + Sequence Listing; English.
XA
XX AAK54951 to AAK64702 encode the human Immune/Haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (II)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (II)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat Immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human Immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 14969 BP; 4016 A; 3069 C; 3042 G; 4842 T; 0 other;

Alignment Scores:	1.55e-65	Length:	14969
Pred. No.:	737.00	Matches:	172
Score:	37.23%	Conservative:	0
Percent Similarity:	37.23%	Mismatches:	1
Best Local Similarity:	40.97%	Indels:	290
Query Match:	22	Gaps:	1
DB:			
US-09-745-506-37 (1-350) x AAK78763 (1-14969)			
QY	1 MetaspLeuYsAlaLeuLeuSerSerLeuSnaSPheAlaSerLeuSerPheAlaGlu	20	
DB	2604 ATGGATTTGAAGGCTCCCTCTTCTCTTGATAGACTTTGCATCCCTCTGCTTGAG	2663	
OY	21 SerTPraspaSnaValGlyLeuLeuValGluProSerProPronIsthrValAsnThrLeu	40	
DB	2664 AGTTGGGACAAATGTTGGATCTAGCTGGTGAACCAACCCACACATAGTGAATACACTC	2723	
OY	41 PheLeuThrAsnaSPheLeuThrGluGluValMetGluValLeuGluInLysValAsp	60	
DB	2724 TTCTGACCAATGACCTGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2783	
OY	61 LeuIleLeuSerTYrHisProPronIlePheArgProMetLysArgIleThrTPAsnThr	80	
DB	2784 CTCATCTCTCTTACATCCGCTCATCTCTCGGACCACTGAAGCCCATTAAGTGAACACA	2843	
OY	81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTYrSerProHis	100	
DB	2844 TGAAG	2903	
OY	101 ThrAlaTYrAspAlaAlaProGluGlyAlaAsnAsnTrpLeuAlaLysGlyLeu	118	
DB	2904 ACAGCTATGATGCTGCGCCGCCAGGCGCTCAACAACATGTTGGCTAAAGGCT-TGGTGA	2962	
OY	118	118	
DB	2963 GAAGCTCTTTCATATTTGATATTTTCCCTGCAATACCTTGAACCTTTAGAGATGCTTT	3022	
OY	118	118	
DB	3023 CCAAGTAAGTTTAACTGCTTTAGGGTTGGGAGAGGCATGATTCATTTTATATATATA	3082	
OY	118	118	
DB	3083 TTTTAAAAATATGTTGCTGAATTTGGCAGTTAATTCGATTTGAAAAAGGAACATTTT	3142	
OY	118	118	
DB	3143 TTATTTATGAGAGTAAAGAGACAGAAAGTTTCCCTTACTGAGCTGAGCTTCATGATTC	3202	
OY	118	118	
DB	3203 TCACCTTTCGTGGCAATGCTGTGCACCCAGGCACTTGGAAAAATGCTTGTGAATTGAA	3262	
OY	118	118	
DB	3263 GCTAGGCTCTCCAGATACATGATTAAGTCAAGTAATAGACATCAGGGTTTT	3322	
OY	118	118	
DB	3323 AATGATGTTTAAAGTAAATGTTTACTTATGACACAAATGAGGAGATGATGATGGA	3382	
OY	118	118	
DB	3383 TTTTATGCTTTTATTTAGTAACTTTTACTTACTTATTTGGGCTAAAGCTTTTATGATG	3442	
OY	118	118	
DB	3443 ATATCTGATTAATGTGTCAAAATTAAGTATGAGCATTTGCACCTGAATGATGTTTAC	3502	
OY	118	118	
DB	3503 ATGGCTATATTACCAAGCAGTACCACTTCTGTATATATATGAAAAATGATGATGATCAG	3562	

OY	118	-----	118	-----	118
Db	3563	TCCTTCTTGCCAACTTTTCAGAGATTGAAGATCTTTGGAAAAATATTCGAAATA	3622		
OY	118	-----	118	-----	118
Db	3623	ATTGATTTTGTANGTCCATGCCAAAGCCCTAGATTAATGGGAGCTGGATGATATCTA	3682		
OY	118	-----	118	-----	118
Db	3683	AGGAGTGTGTANGTATATGACATGAGATGAATCTTTTAAAAAGCATTTCTTAG	3742		
OY	118	-----	118	-----	118
Db	3743	AAATTTGGCTATATAAGTTACTTTTAATCTTAATCTGCACCCCAAACTCCAT	3802		
OY	119	-----	119	-----	119
Db	3803	TTTCCCAAAATATTTTCTCTGTAGAGCTGTGTACCTCCAGGCCCAACATCTCCAAAGCT	3862		
OY	132	ProspAlyrProthrglUGlyAsnHisArgValGluPheAsnValAsnTyrThrGlnAsp	151		
Db	3863	CCCACTPACCTTACAGAGGGAACCCAGAGTAATTAATTAAGTTACTTACACCCAGAC	3922		
OY	152	LeuAspYsValMetSerAlaValIleGlyIleAspGlyAlaSerValThrSerPheSer	171		
Db	3923	CTGCAACAAGTCATGTCTGCAGTGAAAGAAATTCAGCGGTGTTCTGTACACTTCTTTTCT	3982		
OY	172	AlaArg 173			
Db	3983	GCTAGG 3988			
RESULT 12					
ID	AAAL23953				
	AAAL23953 standard; cDNA; 462 BP.				
AC	AAAL23953;				
XX	07-DEC-2001 (first entry)				
DT					
XX	Human breast cancer expressed polynucleotide 16410.				
DE					
XX	Human; breast cancer; cell marker; cytostatic; ss.				
XX	Homo sapiens.				
OS					
XX	WO200151628-A2.				
PN					
XX	19-JUL-2001.				
PD					
XX	10-JAN-2001; 2001WO-US00798.				
PF					
XX	14-JAN-2000; 2000US-0176077.				
PR	14-MAR-2000; 2000US-0189167.				
PR	24-MAR-2000; 2000US-0192099.				
PR	29-MAR-2000; 2000US-0193480.				
PR	15-MAY-2000; 2000US-0205230.				
PR	09-JUN-2000; 2000US-0211315.				
PR	25-JUL-2000; 2000US-0220534.				
PA					
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.				
XX					
PI	Lillie J, Xu Y, Wang Y, Steinmann K;				
XX					
XX	WPI; 2001-451856/48.				
DR					
XX	New peptide useful as a marker for the diagnosis of breast cancer				
XX					
PS	Claim 1; Page 3004; 3695pp; English.				
XX					
CC	The invention relates to human breast cancer expressed polynucleotides				
CC					

CC	aligned with breast cancer by examining the correlation between the expression of certain markers and encoded polypeptides are potential markers for
CC	The polynucleotides and encoded polypeptides are potential markers for
CC	detecting, diagnosing, monitoring, characterizing, treating and
CC	potentially preventing breast cancer. The polynucleotides and encoded
CC	polypeptides are also useful for isolating compounds with cytostatic
CC	activity.
XX	
SQ	Sequence 462 BP, 103 A, 126 C, 118 G, 115 T, 0 other;
Alignment Scores:	
Pred. No.:	5,04e-58
Score:	644.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	35.80%
DB:	22
	Gaps: 0
US-09-745-506-37 (1-350) x AAL23953 (1-462)	
QY	1 MetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB	96 ATGGATTGGAAAGCGCTCTCTTCCTTGAATGACCTTGACCTCTCGTTCTCTGAG 155
QY	21 SerTPAspAsnValGlyLeuLeuValGluProSerProPheHisThrValAsnThrLeu 40
DB	156 AGTTGGGACAAATGTTGGATTACTGGTGGACCAAGCCACACATACGTAAATACAGTC 215
QY	41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAsp 60
DB	216 TTCCTGACCAATGACCTGACTGAGAAAGATGAGAGAGTCTGCAAAAGAAGCGACAGC 275
QY	61 LeuLeuLeuSerTyrHisProProIlePheArgProMetLysArgIleThrTrpAsnThr 80
DB	276 CTCATTCTCTCTACCATCCGCGCTATCTTCGACCATGAAGCGCTAACTGGAAACACA 335
QY	81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
DB	336 TCGAAGGACCGCTGCTGATCCGGGCTCTGGAGAACAGAGTGGTATCTACTCTCTCAT 395
QY	101 ThrAlaTyrAspAlaAlaProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
DB	396 ACAGCGTATGATGCTCGCGCCAGGGCGTCACAACTGGTGTAAAGGCTTGGAGCT 455
QY	121 CysThr 122
DB	456 TGTACC 461
RESULT 13	
AAL15105	
ID	AAL15105 standard; cDNA, 514 BP.
XX	
AC	AAL15105;
XX	
DT	07-DEC-2001 (first entry)
XX	
DE	Human breast cancer expressed polynucleotide 7562.
XX	
KW	Human; breast cancer; cell marker; cytostatic; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200151628-A2.
XX	
PD	19-JUL-2001.
XX	
PF	10-JAN-2001; 2001MO-US00798.
XX	
PR	14-JAN-2000; 2000US-0176077.
PR	14-MAR-2000; 2000US-0189167.
PR	24-MAR-2000; 2000US-0192099.
PR	29-MAR-2000; 2000US-0193480.
PR	15-MAY-2000; 2000US-0205230.


```

Db      380 TGGGATTAAGAGAGTGGTGGCGTCACGACGTGGCTATTAAGGCAATGATATCATCAGC 439
Qy      123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgVal 142
        |||||::: |||
Db      440 ATCGGCCCTCTGGAACCGGAG----- 460
Qy      143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle 162
        ::: |||
Db      461 -----TTGGGTGCTCTCCCGGT--- 478
Qy      163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThrArgIle 182
        478 ----- 478
Qy      183 AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSerArgAsnLys 202
        478 ----- 478
Qy      203 GlnLeuTyrGlnLysThrGlnIleLeuSerLeuGluLysProLeuLeuHisThrGly 222
        479 -----ACCGGA 484
Qy      223 MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIle 242
        |||||::: |||::: |||||::: |||||:::
Db      485 TCCGCTAGATAT-----ATAGAAACCAAAATGAGAGCTTCCAGAGTGGTGAAGTCTGTG 538
Qy      243 LysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGlu 262
        :::: |||::: |||::: |||||::: |||||:::
Db      539 CAAAAAGCCCATTAAGAAACAGC---GTGCACGTTGCTAGCTGTGGCCACACCCCAAG 595
Qy      263 SerGlnValLysValValAlaLeuCysAlaGlySerGlySerValLeuGlnIleVal 282
        :::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db      596 ACACATCATCCAAATCCGTCGCGCATTTGTGCGGCTGTGAGCATCTCTGTGAAGGATATC 655
Qy      283 GlnAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAlaIleAsp 302
        :::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db      656 CAAGCGGATCTATCATATTACCGCGCAATGTCCTCCATCAGAAAGTCTGAGATTACTCAC 715
Qy      303 GlnGlyIleAsnValIleLeuCysGluHisSerAsnThrGluArgLysPheLeuSerAsp 322
        |||||::: |||||::: |||||::: |||||::: |||||:::
Db      716 AACAAATACCAACCGTCTCTCTGCAATCATTAATTCAGAAAGGTTTCTCCATGAG 775
Qy      323 LeuArgAspMetLeuAspSerHisLeuGluAsnLysIleAsnIleIleLeuSerGlnThr 342
        :::: |||::: |||::: |||::: |||::: |||:::
Db      776 TTTTCCCTATATTTGGCCAAATCTTTAAATGAGAAATGCCGTGATTTGTATCTGAAGTG 835
Qy      343 AspArgAspProLeuGlnValVal 350
        |||||::: |||||::: |||||:::
Db      836 GACAAAGATCTCTGTCACCGCTG 859

```

RESULT 15

ABLI0022 standard; cDNA; 2967 BP.

```

AC      ABLI0022;
XX      26-MAR-2002 (first entry)
DE      Drosophila melanogaster expressed polynucleotide seq ID NO 24548.
XX      KW      Drosophila; developmental biology; cell signalling; insecticide;
        KW      pharmaceutical; gene; ss.
XX      OS      Drosophila melanogaster.
XX      PN      WO200171042-A2.
PD      27-SEP-2001.
XX      23-MAR-2001; 2001WO-US09231.
PF      23-MAR-2000; 2000US-191637P.
PR      11-JUL-2000; 2000US-0614150.

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XX      (PEKE ) PE CORP NY.
PA      Venter JC, Adams M, Li PWD, Myers EW;
XX      WPI: 2001-656860/75.
XX      P-PsDB: ABB65919.
DR      New isolated nucleic acid detection reagent for detecting 1000 or more
        PT      genes from Drosophila and for elucidating cell signalling and cell-cell
        PT      interactions -
        PS      Claim 1; SEQ ID NO 24548; 21pp + Sequence Listing; English.
XX      The invention relates to an isolated nucleic acid detection reagent
        CC      capable of detecting 1000 or more genes from Drosophila. The invention is
        CC      useful in developmental biology and in elucidating cell signalling and
        CC      cell-cell interactions in higher eukaryotes for the development of
        CC      insecticides, therapeutics and pharmaceutical drugs. The invention
        CC      discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA
        CC      sequences (ABLI5737-ABLI2072).
        CC      The sequence data for this patent did not form part of the printed
        CC      specification, but was obtained in electronic format directly from WIPO
        CC      at ftp.wipo.int/pub/published_pct_sequences.
XX      SQ      Sequence 2967 BP; 844 A; 651 C; 669 G; 803 T; 0 other.
        Alignment Scores:
        Pred. No.: 6,18e-50 Length: 2967
        Score: 578.00 Matches: 118
        Percent Similarity: 51.44% Conservative: 61
        Best Local Similarity: 33.91% Mismatches: 81
        Query Match: 32.13% Indels: 88
        DB: 23 Gaps: 4
        US-09-745-506-37 (1-350) x ABLI0022 (1-2967)
Qy      3 LeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTrp 22
        |||||::: |||::: |||::: |||::: |||::: |||
Db      66 CTGGCGGCTGTGGTTCAGAGAGCTGAGAACTTTGCTCCGACTTCTTGGCAGAGAAAGTG 125
Qy      23 AspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThrLeuPheLeu 42
        |||||::: |||||::: |||||::: |||||::: |||||:::
Db      126 GACAAATGTGGACTCTCATATCGAACCGCGCAAAACAAATACAAATATCTATTATTA 185
Qy      43 ThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysLysAlaAspLeuIle 62
        |||||::: |||||::: |||||::: |||||::: |||||:::
Db      186 ACTAAGATTTATACCGAGCCCGCTAGTAAGAAGCGCTAAGAGAGAGCGGAGCTCTATA 245
Qy      63 LeuSerTyrHisProIlePheArgProMetLysArgIleThrTrpAsnThrTrpLys 82
        :::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db      246 ATCAGCTATCATCCGCCAATTTTCAAGCCCGTACAGAGATATACCATCATTCGCAAG 305
Qy      83 GluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHisThrAla 102
        |||||::: |||::: |||::: |||::: |||::: |||
Db      306 GAGCGCGTGTGGCAGCATGCTTGGCCAACGATATAGCCTGTACTGCGCCACACGCGG 365
Qy      103 TyrAspAlaAlaProGlnIlyValAsnAsnTrpLeuAlaLysGlyLeuGlyValAcysThr 122
        :::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db      366 TGGGATTAAGACAGAGTGGCGCTCAACGATGCGTATTAAGCAGTGAATATCTACAGC 425
Qy      123 SerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlyAsnHisArgVal 142
        |||||::: |||::: |||::: |||::: |||::: |||
Db      426 ATCGGCCCTCTGGAACCGGAG----- 446
Qy      143 GluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIle 162
        :::: |||::: |||::: |||::: |||::: |||:::
Db      447 -----TTGGGTGCTCTCCCGGT--- 464
Qy      163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGlnThrArgIle 182
        464 ----- 464

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OY 183 AsnLeuAsnCysThrGlnIysAlaLeuMetGlnValValAspPheLeuSerArgAsnIys 202
Db 464 ----- 464
OY 203 GlnLeuTyrGlnIysThrGlnIleLeuSerLeuGlnIysProLeuLeuHisThrGly 222
Db 465 -----ACCGGA 470
OY 223 MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIle 242
Db 471 TCCGGTAGATAT-----ATAGAAACCAAAATGAGACTTCCACAGGTGTGAGTCTCTG 524
OY 243 LysArgHisLeuIysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGlu 262
Db 525 CAAAGCCGATTAGAAACAGC--GTGCACGTTGCTGTAGCTGTGGGCCACACCCCAAG 581
OY 263 SerGlnValIysValValAlaLeuCysAlaGlySerGlySerSerValLeuGlnIysVal 282
Db 582 ACACATCATCCAAATCCGCGCATTTGTGCGGCTCTGGAGCATCTCTGTGAAGGATATC 641
OY 283 GluAlaAspLeuTyrLeuThrGlyGluMetSerHisHisAspThrLeuAspAlaIleSer 302
Db 642 CAGCGGATCTTATCATTAACCGCGAAATGTCCCATCAGCAAGTCTGTGAGTTACTCAC 701
OY 303 GlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGlnArgGlyPheLeuSerAsp 322
Db 702 AACATATACCAACCGTTCTTCTCTGCATCATAGTATATTCAGAAAGGGTATTCTCCATGAG 761
OY 323 LeuArgAspMetLeuAspSerHisIleGluAsnIysIleAsnIleIleLeuSerGluThr 342
Db 762 TTTTGCCCTATATGGCCAAATCTTAAATGAAGAATGCCCTGATTTGTATCTGAAGTG 821
OY 343 AspArgAspProLeuGlnValVal 350
Db 822 GACAAAGATCTCTGTGTCACCGTG 845
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Job time : 274 secs

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